

GenCore version 4.5

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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:17:16 ; Search time 52.57 Seconds

(without alignments)

147.151 Million cell updates/sec

Title: US-09-331-631A-24_COPY_29_94

Perfect score: 382

Sequence: 1 HDDEDRRGHSLQQCVCQRC.....EQEBEQGRGRGWHGEGEREE 66

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL15; *
 1: sp_archaea:*
 2: sp_bacteria:*
 3: sp_fungi:*
 4: sp_human:*
 5: sp_invertebrate:*
 6: sp_mammal:*
 7: sp_mhc:*
 8: sp_organelle:*
 9: sp_Phage:*
 10: sp_Plant:*
 11: sp_Rodent:*
 12: sp_Virus:*
 13: sp_vertebrate:*
 14: spUnclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

ALIGNMENTS

RESULT	1
ID	Q03678
AC	Q03678;
DT	01-NOV-1996 (TREMBLrel. 01, Created)
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	FETAL SPORGE PROTEIN.
GN	BEG1 OR GBL1.
OS	Hordeum vulgare (Barley), and Triticum aestivum (Wheat).
OC	Eukaryota; Viridiplantae; Embryophyta; tracheophyta; spermatophyta;
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Hordeum.
NCBI_TAXID	4513, 4565;
RN	{1}
RP	SEQUENCE FROM N.A.
RX	MEDLINE-9328798; PubMed=8510647;
RA	Heck G.R., Chamberlain A.C., Ho T.H.D.;
RT	"Barley embryo globulin 1 gene, Beg1: characterization of cDNA, chromosome mapping and regulation of expression.";
RL	Chrom. Gen. 23(9):209-212(1993).
DR	M1-2936; AAU32936; 1; -.
DR	M1-2936; AAU32936; 1; -.
DR	EMBL; M64372; AAU32936; 1; -.
DR	EMBL; M81719; AAU34269; 1; -.
DR	HSSP; P02853; 2PHL.
DR	MENDEL; 8553; Horvut; 1188; 8553.
DR	INTERPRO; IPR000501; -.
DR	INTERPRO; IPR001113; -.
DR	PFAM; PF00546; Seedstore_7s; 1.
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
DR	PRODOM; PD081059; -; 1.
KW	Seed storage protein.
SEQUENCE	637 AA; 72252 MW; F323F4FF9947C3C CRC64;

Query Match Best Local Similarity 100.0%; Score 382; DB 10; Length 637; Matches 66; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Result No.	Score	Query	Match length	DB ID	Description
1	382	100.0	637	10	Q03678
2	138	66.1	582	10	Q03685
3	136	35.6	238	10	Q03625
4	135	35.3	238	10	Q03624
5	135	35.3	238	10	Q03625
6	135	35.3	238	10	Q03626
7	135	35.3	240	10	Q03627
8	135	35.3	240	10	Q03628
9	135	35.3	242	10	Q03629
10	135	35.3	242	10	Q03630
11	135	35.3	407	10	Q03631
12	134	35.1	238	10	Q03632
13	134	35.1	238	10	Q03633
14	133	34.8	238	10	Q03634
15	133	34.8	240	10	Q03635
16	133	34.8	240	10	Q03636
17	133	34.8	240	10	Q03637
18	133	34.8	540	10	Q03638
19	132	34.6	239	10	Q03639

Db	89	 EGERE 94	DR PF00546; Seedstore_7s; 1 PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
RESULT	2		
ID	Q03865	PRELIMINARY; PRT; 582 AA.	
AC	003865;		
DT	01-NOV-1996 (TREMBLrel. 01, Created)		
DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	VICILIN-LIKE EMBRYO STORAGE PROTEIN.		
GN	GLOB1-L.		
OS	zea mays (Maize).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.		
OX	NCBI_TaxID=4577;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	STRAIN=W64A;		
RX	MEDLINE=92080707; PubMed=1752424;		
RA	Belanger F.C.; Kriz A.L.;		
RT	"Molecular basis for allelic polymorphism of the maize Globulin-1 gene.";		
RL	Genetics 129:863-872(1991).		
DR	EMBL: X59033; CAA41809.1; -.		
DR	HSFP; P50477; ICAU.		
DR	MENDEL; 1134; Zeama; 1188; 11234.		
DR	INTERPRO; IPR000901; -.		
DR	INTERPRO; IPR00113; -.		
DR	PFAM; PF00546; Seedstore_7s; 1.		
DR	PRODOM; PD081059; -; 1.		
KW	Seed Storage protein.		
SEQUENCE	582 AA; 66162 MW; 680D85FECB7CB885 CRC64;		
Query Match	36.1%; Score 138; DB 10; Length 582;		
Best Local Similarity	37.7%; Pred. No. 2e-08;		
Matches	26; Conservative 14; Mismatches 21; Indels 8; Gaps 3;		
Qy	2 DDEDDRGGHSLOQCVCORCROERPRVSHARCVQECRDO---QQHGRHEEPEEQGRG 57		
Db	26 DNNHHHHGGHKSQCVRRC-EDRPWHORPRLQECREERERKQRERSRHEADRSSEG- 82		
Qy	58 WHGEGEREE 66		
Db	83 -SSEDEREQ 90		
RESULT	3		
ID	081257	PRELIMINARY; PRT; 238 AA.	
AC	081257;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)		
DE	GLOBULIN-1 (FRAGMENT).		
OS	Zea Luxurians (Teosinte).		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.		
OX	NCBI_TaxID=15945;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RA	Hilton H., Gaut B.S.;		
RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";		
RL	Genetics 0:0-0(1998).		
DR	EMBL; AF064212; AAC31455.1; -.		
DR	HSFP; P50477; ICAU.		
DR	MENDEL; 31891; Zeama; 1188; 31891.		
DR	INTERPRO; IPR000901; -.		
DR	INTERPRO; IPR00113; -.		
DR	PFAM; PF00546; Seedstore_7s; 1.		
DR	PROSITE; PS00867; CPASE_2; UNKNOWN_1.		
FT	NON_TER 238; 238		
SQ	SEQUENCE 238 AA; 27298 MW; EDF6A1DE3F86D0F0 CRC64;		
Query Match	35.3%; Score 135; DB 10; Length 238;		
Best Local Similarity	36.2%; Pred. No. 2e-08;		
Matches	25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;		
Qy	2 DDEDDRGGHSLOQCVCORCROERPRVSHARCVQECRDO---QQHGRHEEPEEQGRG 57		
Db	26 DNNHHHHGGHKSQCVRRC-EDRPWHORPRLQECREERERKQRERSRHEADRSSEG 84		
Qy	58 WHGEGEREE 66		
Db	85 EDEREREQ 92		
RESULT	5		
ID	081255	PRELIMINARY; PRT; 238 AA.	
AC	081255;		
DT	01-NOV-1998 (TREMBLrel. 08, Created)		
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)		
DE	GLOBULIN-1 (FRAGMENT).		
OS	Zea mays subsp. parviflum.		
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;		
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.		
OX	NCBI_TaxID=76912;		

RN	[1]	AC	Q9SBP0;
RP	SEQUENCE FROM N.A.	DT	01-MAY-2000 (TREMBLrel. 13, Created)
RA	Hilton H., Gaut B.S.;	DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";	DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
RL	Genetics 0:0-0(1998).	DE	GLOBULIN-1 (FRAGMENT).
DR	EMBL: AF054224; AAC31467.1; -.	OS	zea mays subsp. <i>Parviflumis</i> .
DR	MENDEL; 31897; Zeama; 1180; 31897.	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
DR	INTERPRO; IPR000901; -.	OC	Magnoliophyta; Liliopsida; Poales; Poaceae; zea.
DR	INTERPRO; IPR001113; -.	OX	NCBITaxonID:76912;
DR	PFAM; PF00546; Seedstore_7s; 1.	RN	[1]
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.	RP	SEQUENCE FROM N.A.
FT	NON_TER 238 AA; 238 MW; 1186EA5D6EEB507E CRC64;	RA	Hilton H., Gaut B.S.;
SQ	SEQUENCE	RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";
Query Match	35.3%; Score 135; DB 10; Length 238;	RT	Genetics 0:0-0(1998).
Best Local Similarity	38.2%; Pred. No. 2e-08;	RL	EMBL: AF064219; AAC31462.1; -.
Matches	26; Conservative 13; Mismatches 21; Indels 8; Gaps 3;	DR	HSSP; P50477; ICAU
Qy	2 DDEDRRGHSLQOCVQRCRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGKG 57	DR	INTERPRO; IPR000901; -.
Db	26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84	DR	INTERPRO; IPR001113; -.
Qy	58 WHGGERE 65	DR	PFAM; PF00546; Seedstore_7s; 1.
Db	83 -SSEDERE 89	DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
RESULT	6	SQ	SEQUENCE
Q9SBP8	PRELIMINARY; PRT; 238 AA.	Query Match	35.3%; Score 135; DB 10; Length 240;
ID	Q9SBP8	Best Local Similarity	36.2%; Pred. No. 2.1e-08;
AC	Q9SBP8;	Matches	25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;
DT	01-MAY-2000 ("TREMBLrel. 13, Created")	Qy	2 DDEDRRGHSLQOCVQRCRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGKG 57
DT	01-MAY-2000 ("TREMBLrel. 13, Last sequence update")	Db	26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84
DT	01-OCT-2000 ("TREMBLrel. 15, Last annotation update")	Qy	58 WHGGERE 66
DE	GLOBULIN-1 (FRAGMENT).	Db	85 -EDREREQ 92
OS	zea mays subsp. <i>parviflumis</i> .	RESULT	8
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;	ID	Q9SBP9
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; zea.	AC	Q9SBP9;
NCBI_TAXID=76912;	[1]	DT	01-MAY-2000 ("TREMBLrel. 13, Created")
RN	SEQUENCE FROM N.A.	DT	01-MAY-2000 ("TREMBLrel. 13, Last sequence update")
RP	RA Hilton H., Gaut B.S.;	DT	01-OCT-2000 ("TREMBLrel. 15, Last annotation update")
RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";	DE	GLOBULIN-1 (FRAGMENT).
RT	Genetics 0:0-0(1998).	OS	zea mays subsp. <i>parviflumis</i> .
RL	EMBL; AF064221; AAC31464.1; -.	OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
DR	HSSP; P50477; ICAU	OC	Magnoliophyta; Liliopsida; Poales; Poaceae; zea.
DR	INTERPRO; IPR000901; -.	OX	NCBITaxonID:76912;
DR	INTERPRO; IPR001113; -.	RN	[1]
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.	RP	SEQUENCE FROM N.A.
FT	NON_TER 238 AA; 238 MW; A75C0C/D8D9B773A CRC64;	RA	Hilton H., Gaut B.S.;
SQ	SEQUENCE	RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene.";
Query Match	35.3%; Score 135; DB 10; Length 238;	RT	Genetics 0:0-0(1998).
Best Local Similarity	36.2%; Pred. No. 2e-08;	DR	EMBL; AF064220; AAC31463.1; -.
Matches	25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;	DR	HSSP; P50477; ICAU
Qy	2 DDEDRRGHSLQOCVQRCRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGKG 57	DR	INTERPRO; IPR000901; -.
Db	26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84	DR	INTERPRO; IPR001113; -.
Qy	58 WHGGERE 66	DR	PFAM; PF00546; Seedstore_7s; 1.
Db	85 -EDREREQ 92	DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
RESULT	7	FT	NON_TER 240 AA; 27492 MW; ECC26326633DFFB9 CRC64;
Q9SBP0	PRELIMINARY; PRT; 240 AA.	SQ	SEQUENCE
Query Match	35.3%; Score 135; DB 10; Length 240;	Query Match	35.3%; Score 135; DB 10; Length 240;
Best Local Similarity	36.2%; Pred. No. 2.1e-08;	Best Local Similarity	36.2%; Pred. No. 2.1e-08;
Matches	25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;	Matches	25; Conservative 16; Mismatches 22; Indels 6; Gaps 3;
Qy	2 DDEDRRGHSLQOCVQRCRQERPRYSHARCVQCRDD---QQQHGRHEQQEEQGRGKG 57	Db	26 DDNHHHHGGHKSGRCVRRC-EDRPWHQRPRCLQCREERERKRSRHEADRSKGSS 84

DR	HSSP; P50477; ICAU
DR	INTERPRO; IPR000901; -
DR	INTERPRO; IPR01113; -
DR	PFAM; PF05546; Seedstore_7s; 1
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FRT	NON_TER 238
SQ	SEQUENCE 238 AA; 27254 MW; FFEK7BA7B4A25D68 CRC64;
DB	83 -SSEDREQ 90
RESULT	13
09S6Z6	PRELIMINARY; PRT; 238 AA.
09S6Z6	AC 09S6Z6; 01-MAY-2000 (TREMBLrel. 13, Created)
DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	GLOBULIN-1 (FRAGMENT).
OS	zea luxurians (Teosinte).
OC	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC	Magnoliophyta; Liliopsida; Poales; Poaceae; Zea.
NCBI_TAXID	15945;
RN	[1] SEQUENCE FROM N.A.
RA	Hilton H., Gaut B.S.;
RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene."; Genetics 0:0-0 (1998).
RL	Genetics 0:0-0 (1998).
DR	EMBL; AF054232; AAC31475.1; -.
DR	EMBL; AF064227; AAC31470.1; -.
DR	EMBL; AF064230; AAC31473.1; -.
DR	HSSP; P50477; ICAU.
DR	INTERPRO; IPR000901; -.
DR	INTERPRO; IPR00113; -.
DR	PFAM; PF00546; Seedstore_7s; 1
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT	NON_TER 238 AA; 27271 MW; FFE2169616319268 CRC64;
SQ	SEQUENCE 238 AA; 27271 MW; FFE2169616319268 CRC64;
Query Match	35.1%; Score 134; DB 10; Length 238; Best Local Similarity 36.2%; Pred. No. 2.7e-08; Mismatches 25; Conservative 15; Indels 8; Gaps 3; Matches 25; Conservative 15; Mismatches 21; Indels 8; Gaps 3;
QY	2 DDEDRRGHSLQOCVQRQERPRYSHARCVQECRDO---QQHGRHEQEEQGRGRG 57
Db	26 DDNHHHGGHKSGRCVVRCC-EDRPWHQRPRCLQCREERERKQERSRHEADRSSEG- 82
Db	58 WHGEGERE 66
Db	83 -SSEDREQ 90
RESULT	14
081258	PRELIMINARY; PRT; 238 AA.
AC	081258; 01-NOV-1998 (TREMBLrel. 08, Created)
DT	01-NOV-1998 (TREMBLrel. 08, Last sequence update)
DT	01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE	GLOBULIN-1 (FRAGMENT).
DR	Hilton H., Gaut B.S.;
RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene."; Genetics 0:0-0 (1998).
RL	Genetics 0:0-0 (1998).
RA	Hilton H., Gaut B.S.;
RT	"Speciation and domestication in maize and its wild relatives: evidence from the Globulin-1 gene."; Genetics 0:0-0 (1998).
DR	EMBL; AF064215; AAC31458.1; -.
DR	HSSP; P50477; ICAU.
DR	MENDEL; 31894; Zeema; 1188; 31894.
DR	INTERPRO; IPR000901; -.
DR	PFAM; PF00546; Seedstore_7s; 1
DR	PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
FT	NON_TER 240 AA; 27560 MW; 5F54BC5CB06A983D CRC64;
SQ	SEQUENCE 240 AA; 27560 MW; 5F54BC5CB06A983D CRC64;
Query Match	34.8%; Score 133; DB 10; Length 240; Best Local Similarity 36.2%; Pred. No. 3.5e-08; Mismatches 25; Conservative 15; Mismatches 23; Indels 6; Gaps 3; Matches 25; Conservative 15; Mismatches 23; Indels 6; Gaps 3;
QY	2 DDEDRRGHSLQOCVQRQERPRYSHARCVQECRDO---QQHGRHEQEEQGRGRG 57
Db	26 DDNHHHGGHKSGRCVVRCC-EDRPWHQRPRCLQCREERERKQERSRHEADRSSEGSS 84
Db	58 WHGEGERE 66
Db	85 -EDERERE 92

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Job time: 454 sec